Add-On Event Descriptions

Please see more information in ASHG's Online Planner, available in June.

Receptions & Luncheons

Trainee Reception (open to trainee and early career attendees only)
Wednesday, November 1: 7:30 pm – 9:30 pm

This fun event on the first night of the meeting, Wednesday, November 1, provides an opportunity to network with other trainees and get advice from potential mentors at different career stages. Enjoy getting to see and meet one another at ASHG while enjoying beverages, food, and games! **Advance ticket purchase required to attend.**

Diversity, Equity, and Inclusion Luncheon
Thursday, November 2: 12:15 pm – 1:45 pm

The Diversity, Equity, and Inclusion Luncheon being held on Thursday, November 2 provides an exceptional venue for networking and showcasing ASHG programs and partnerships focused on advancing diversity, equity, and inclusion in human genetics and genomics. The topic and speaker details will be available in the online planner in June. **Advance ticket purchase required to attend.**

Diversity, Equity, and Inclusion Reception
Thursday, November 2: 7:30 pm – 9:30 pm

The Diversity, Equity, and Inclusion Reception scheduled for Thursday, November 2, will recognize and celebrate the importance of diversity, equity, and inclusion, as well as provide networking for the research and training community. **Advance ticket purchase required to attend.**

Race, Ancestry, Both, or Neither?: Introducing Frameworks for Population Descriptors in Genomics Research
Friday, November 3: 12:15 pm – 1:45 pm

This ticketed lunch session to be held on Friday, November 3, introduces junior investigators and trainees to emerging questions and strategies for considering whether, why, and when to use population descriptors in genomics research. A new report from the National Academies of Sciences, Engineering, and Medicine, *Using Population Descriptors in Genetics and Genomics Research: A New Framework for an Evolving Field*, raised awareness about misuses and highlighted key areas for potential actions across organizations and sectors. How can researchers begin to rethink their own assumptions and integrate new frameworks into different types of research studies? What can departments do to help trainees begin to explore these questions? Join NASEM committee members, researchers, and educators in this roll-up-our-sleeves session to consider and rethink how and why we use race, ethnicity, and ancestry labels in genomics research. **Advance ticket purchase required to attend.**

ASHG's 75th Anniversary Gala Celebration
Saturday, November 4: 7:00 pm – 10:00 pm

Join us for a special closing gala reception at the ASHG 2023 Annual Meeting honoring the Society's 75th Anniversary on Saturday, November 4, 7:00 pm - 10:00 pm at the Ronald Reagan Building and International Trade Center. Themed "One Humanity, Many Genomes," the event will spotlight 75 years of innovation in the field and how genetics and genomics research is generating benefits for people everywhere. The evening will include drinks, food, and live music from Ethidium Spill featuring ASHG members Francis Collins, Anthony Antonellis, and Elliott Marguilies. Join us in celebrating human genetics, our research community, and Society's bright future leading new discoveries and better health for people everywhere. **Advance ticket purchase required to attend. See additional info here.**

Workshops

Teaching Variant Curation Through Team-based, Active Learning Approaches
Wednesday, November 1: 11:00 am – 1:00 pm

Single nucleotide variant (SNV) curation is an important skill to develop for students in genetic counseling, genomics, and bioinformatics master's programs. It is also a common subject for continuing education workshops for professionals working in clinical genetics roles. While the number of evidence categories and scoring criteria can be intimidating for new learners, the process lends itself well to team-based, active learning approaches in the classroom. This workshop will use the ACMG/AMP standards and guidelines for germline SNV interpretation as a case study for developing classroom activities that engage learners, develop variant analysis skills, and build confidence in the curation process for students. Throughout the workshop, participants will gain hands-on experience designing instructional activities for clinical genetics concepts, assessing the effectiveness of the activities, and constructing an instructional scaffold to guide learners to mastery of the curation process. Participants will also discuss the benefits of teaching in a team-based, active modality. While the workshop will focus on in-person educational formats, there will also be discussion of how to adapt the same activities to synchronous, online delivery and self-paced, solo learners. **Advance ticket purchase required to attend.**

Genomic Analysis in the All of Us Researcher Workbench
Wednesday, November 1: 11:00 am – 1:00 pm

The NIH's All of Us Research Program is committed to the ambitious mission of collecting multiple types of health data from a million or more participants to create a diverse research resource that accelerates precision medicine. The All of Us Researcher Workbench is a secure, cloud-based platform where registered researchers access and analyze data from over 413,000 program participants. Of these participants we will have released >245,000 whole genome sequenced samples and >314,000 genotyping arrays in the All of Us Researcher Workbench by Spring of 2023. By Fall of 2023, we also anticipate the availability of the first set of long read genome sequencing data. This genomic data is combined with many types of phenotypic and auxiliary data types including electronic health records, survey data, physical measurements, mobile health data (Fitbit). This free-to-access platform is also a space where researchers have the ability to work collaboratively with other registered researchers through shared workspaces. In addition to increasing the number of samples available to researchers since its launch of genomic data in March 2022, the All of Us program has expanded the resources

available for researchers to explore the genomic data. All of Us has both added new analysis tools, such as REGENIE, and expanded the data types it provides by introducing structural variant datasets from 10,000 participants and 1,000 long read samples in Spring 2023. A main goal of the program is to make this data accessible to a broad array of researchers. The evolution of genomic research is transforming the treatment of disease, motivating wellness and health promotion, and modernizing disease prevention in public health. This workshop invites participation from researchers interested in learning how to utilize the All of Us dataset and Researcher Workbench for their own research. This session will present an overview of the Researcher Workbench, highlighting the expanded data with the Spring 2023 release and then 1) provide an interactive, guided demonstration of the Researcher Workbench, 2) provide participants a hands-on opportunity to replicate a research study with genomics data using newly added tools within the Workbench, 3) conduct an interactive Q&A session to engage attendees about All of Us Researcher Workbench and the novel technology implemented to conduct genomic analyses, and 4) discuss the approach to scale genomics analysis to 1 million participants. **Advance ticket purchase required to attend.**

Using UK Biobank to Scale up your Research
Wednesday, November 1: 2:00 pm – 4:00 pm

Biobank scale datasets have become an important part of nearly all aspects of health research. By systematically linking health outcomes to genetic and other molecular measurements at a previously impossible scale, they enable researchers around the world to carry out well-powered experiments. This workshop will offer a hands-on demonstration of some of the issues that may confront first-time users of these enormous resources, including:

- How to interpret and parse medical outcome data from self-reported assessments, hospital in-patient records, primary care data and other sources. We will demonstrate using an example disease how combining data from different sources substantially increases the power to conduct human disease studies.
- How to work with 'omics data at this scale. We will use the recently released nuclear magnetic resonance (NMR) metabolomic biomarker dataset to show how additional data types can supplement genotype-phenotype studies.
- What kind of biases are important to consider in genetic data in hundreds of thousands of samples that are different from smaller studies, and how to use thorough quality control procedures and robust statistical methods to mitigate these.

We will use the UK Biobank (https://www.ukbiobank.ac.uk/) to demonstrate these issues, as it has excellent data availability, and can be useful to the widest possible range of new users. The session will be delivered primarily through interactive Jupyter notebooks, allowing researchers to follow along at their own pace or alongside the instructors. These will be available both in R and Python. We will use mock data and summary statistics similar in structure to UKBB. We will provide all the materials, including simulated datasets, prior to the session, and those will be available online. **Advance ticket purchase required to attend.**

Reference:
https://www.ukbiobank.ac.uk/enable-your-research/approved-research/biomarker-profiling-by-nmr-metabolomics-for-the-study-of-chronic-disease-risk-and-underlying-risk-factors
https://www.ukbiobank.ac.uk/enable-your-research/about-our-data/health-related-outcomes-data

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The Michigan Imputation Server: Data Preparation, Genotype Imputation, and Data Analysis
Wednesday, November 1: 2:00 pm – 4:00 pm

Genotype imputation is a key component of modern genetic association studies. The Michigan Imputation Server has thus far helped > 9,500 researchers from around the world to impute > 95M human genomes. This interactive workshop is intended for anyone interested in learning how to impute genotypes and to use the imputed genotypes, highlighting recent reference panels, including the multi-ancestry panel from the TOPMed program and a specialized HLA panel. A brief overview of imputation and the server will be followed by demonstrations and exercises, including: 1) quality control and preparation of genetic data for use on the MIS with a special focus on diverse ancestries, chromosome X, and the HLA region; 2) tracking runs and use of the application program interface for larger jobs; 3) downloading data from the MIS and preparing data for genetic analysis; 4) performing a GWAS using imputed data (including HLA region) and interpreting results, taking into account imputation quality; 5) using the additional features, such as the polygenic risk score calculation. We encourage participants to ask specific questions about their own projects. Workshop materials, including slides and example data sets, will be made available before the workshop and will remain online at the MIS website. We expect that this workshop will enable participants to generate high-quality imputed data sets and to effectively analyze them. **Advance ticket purchase required to attend.**

The Confidence Factor: Thriving in Your Career
Friday, November 3: 12:15 pm – 1:45 pm

This panel event designed for early career professionals seeking to gain confidence and unlock their career potential. During this 90-minute session, you'll hear from 3 experienced professionals in genetics who will share their personal journeys to gaining confidence, as well as practical tips for achieving your career goals. The event will feature both panel presentations and round table speed discussions, allowing you to connect with your peers and gain insights into the connection between confidence and success. **Advance ticket purchase required to attend.**

Behind-the-Scenes: Publications Workshop
Saturday, November 4: 12:00 pm – 1:00 pm

This workshop being held on Saturday, November 4, will provide you with information to help navigate the scientific publication process. Editors from multiple journals, including *AJHG* and *HGG Advances*, will give you a behind-the-scenes view of scientific publishing, covering topics such as data sharing, open access publication, and the ins and outs of the peer review process. There will be plenty of time for questions and networking. This session is geared towards trainees and junior faculty who are relatively new to publishing. **Advance ticket purchase required to attend.**